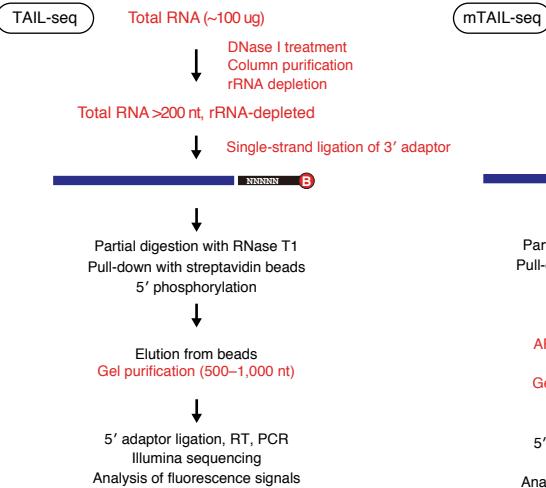
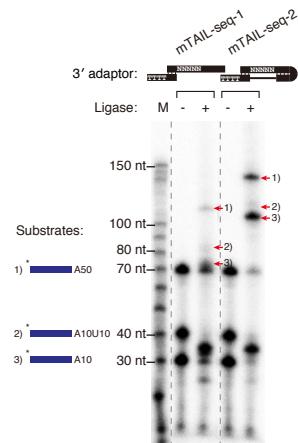


Lim_FigS1

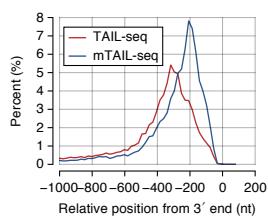
A Comparison of TAIL-seq protocols



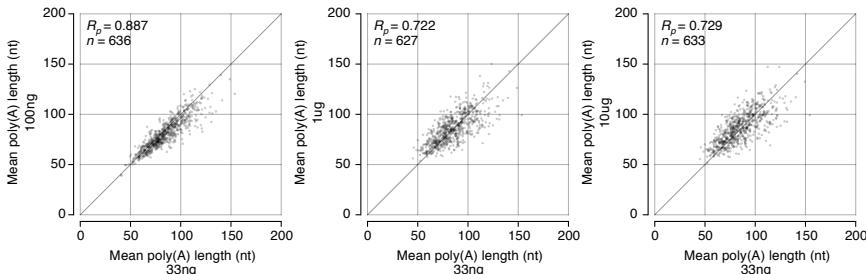
B Ligation efficiency



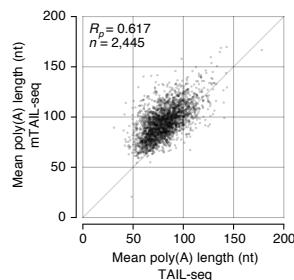
C Position of the 5' end of read 1 relative to the annotated 3' end



D Reproducibility



E Poly(A) tail length comparison



F Capturing uridylated tails

